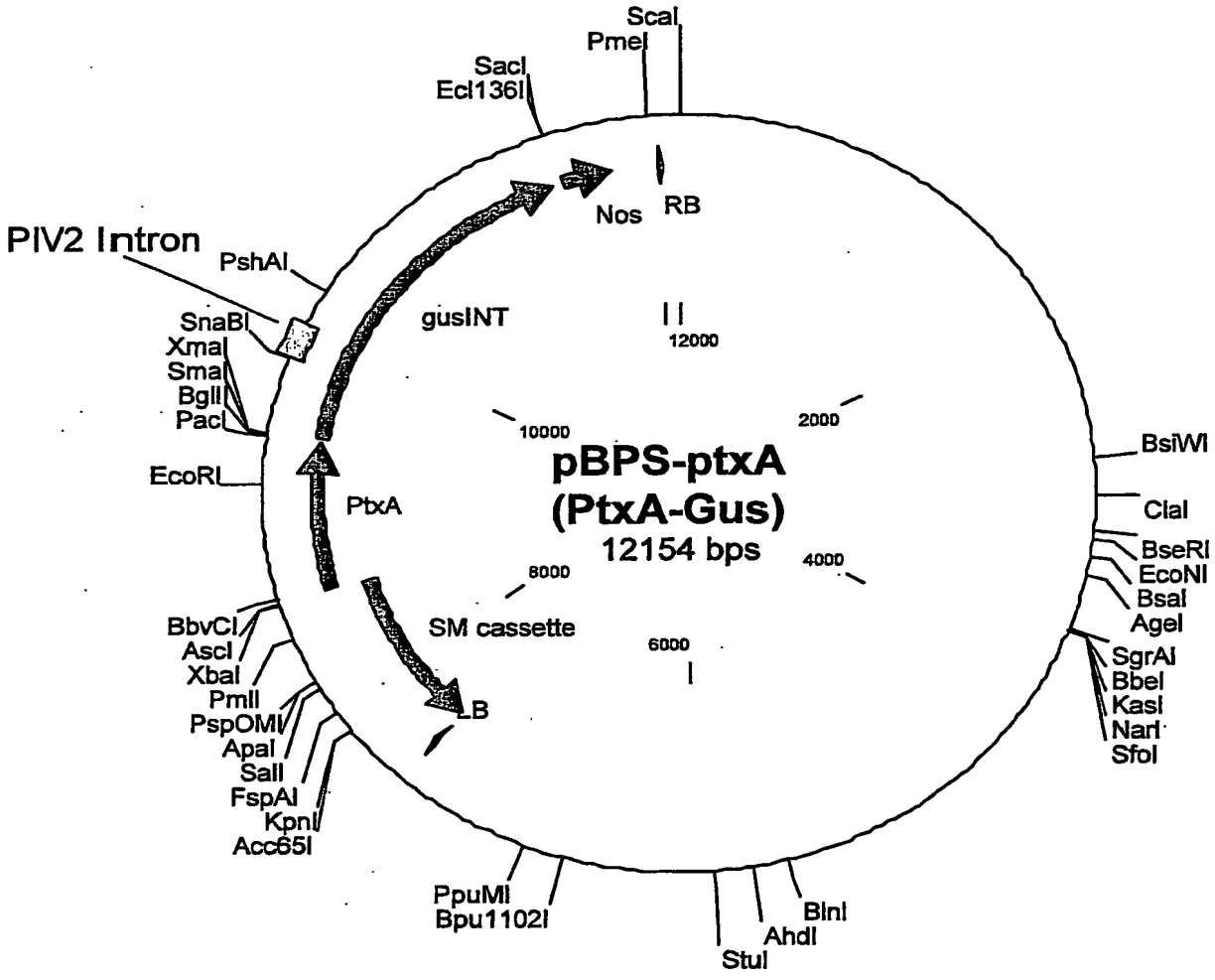
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SacI
Ecl136I
Nos
RB
PIV2 Intron
PshAI
gusINT
SnaBI
XmaI
SmaI
BglII
PacI
12000
10000
2000
pBPS-ptxA
(PtxA-Gus)
12154 bps
EcoRI
PtxA
BsiWI
ClaI
BseRI
EcoNI
BsaI
AgeI
8000
4000
SM cassette
6000
BbvCI
AscI
XbaI
PmlI
PspOMI
ApaI
SalI
FspAI
KpnI
Acc65I
B
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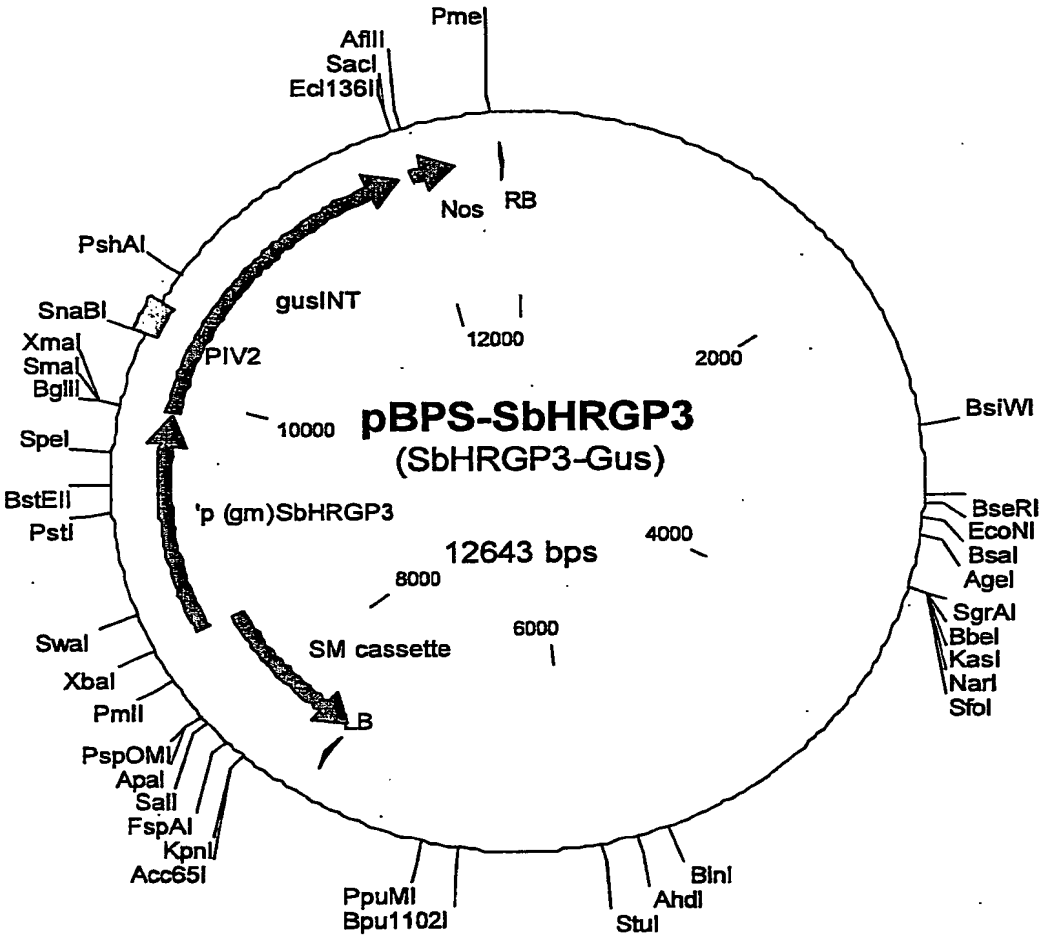
BbeI
KasI
NarI
SfoI
PpuMI
Bpu1102I
BlnI
AhdI
StuI

Fig. 1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(SbHRGP3-Gus)
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Pme
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SacI
Ecl136II
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PshAI
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XmaI
SmaI
BglII
SpeI
BstEII
PstI
SwaI
XbaI
PmlI
PspOMI
ApaI
SalI
FspAI
KpnI
Acc65I
PpuMI
Bpu1102I
StuI
BlnI
AhdI
BsiWI
BseRI
EcoNI
BsaI
AgeI
SgrAI
BbeI
KasI
NarI
SfoI
gusINT
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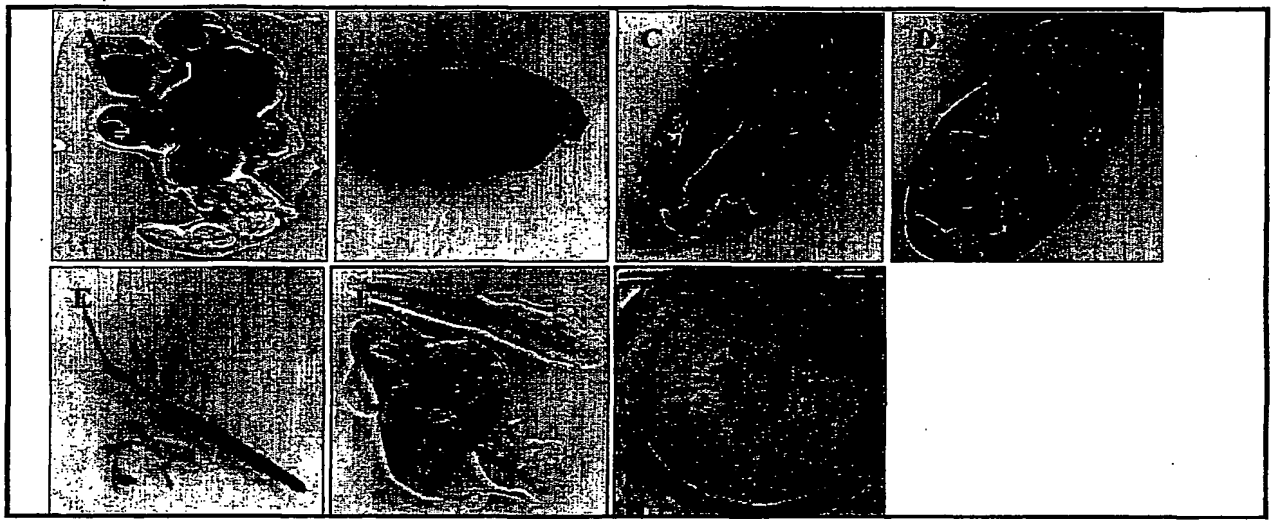
'p (gm)SbHRGP3
SM cassette
B
2000
4000
6000
8000
10000
12000

Fig. 2

I



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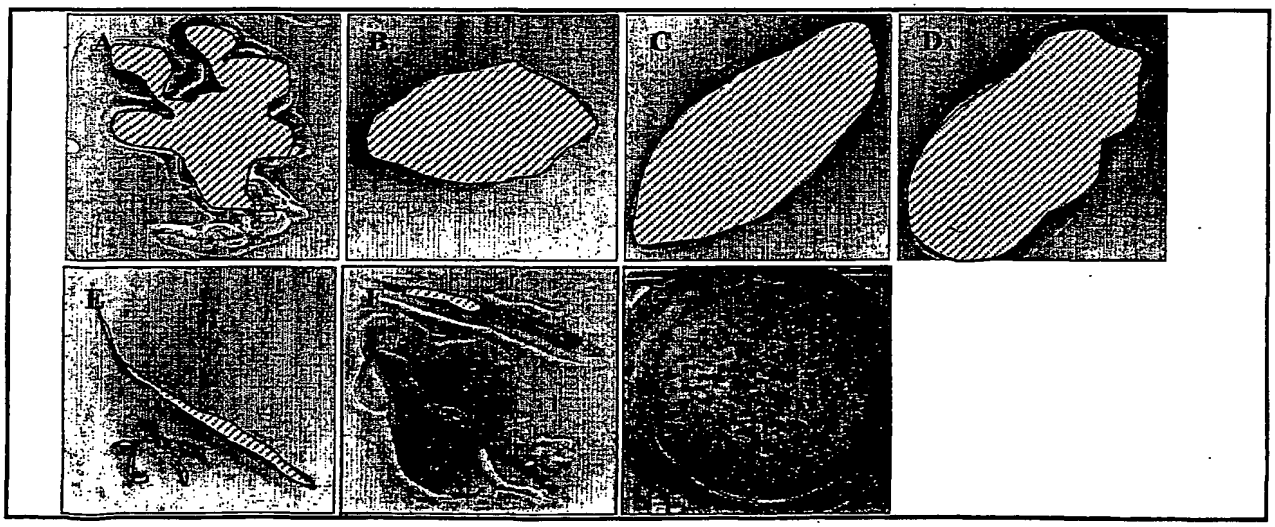
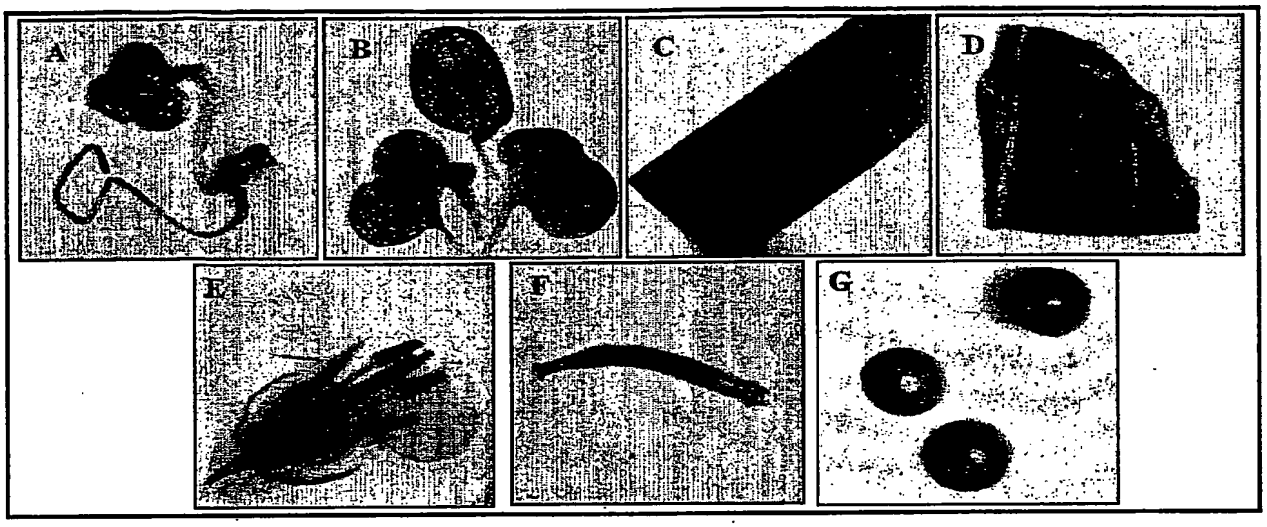


Fig 3

I



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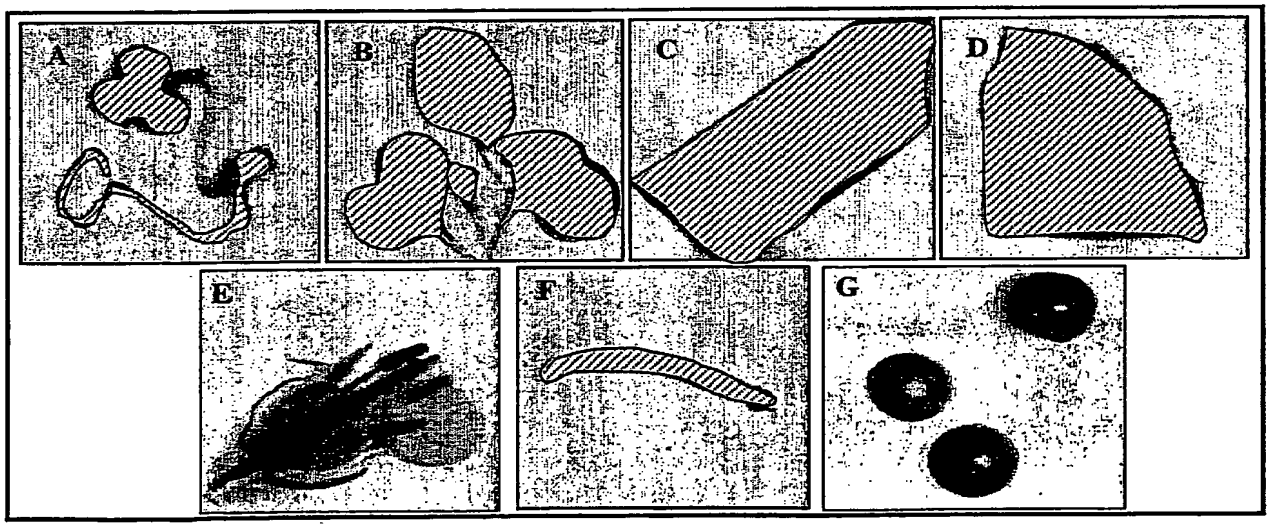

Fig 4

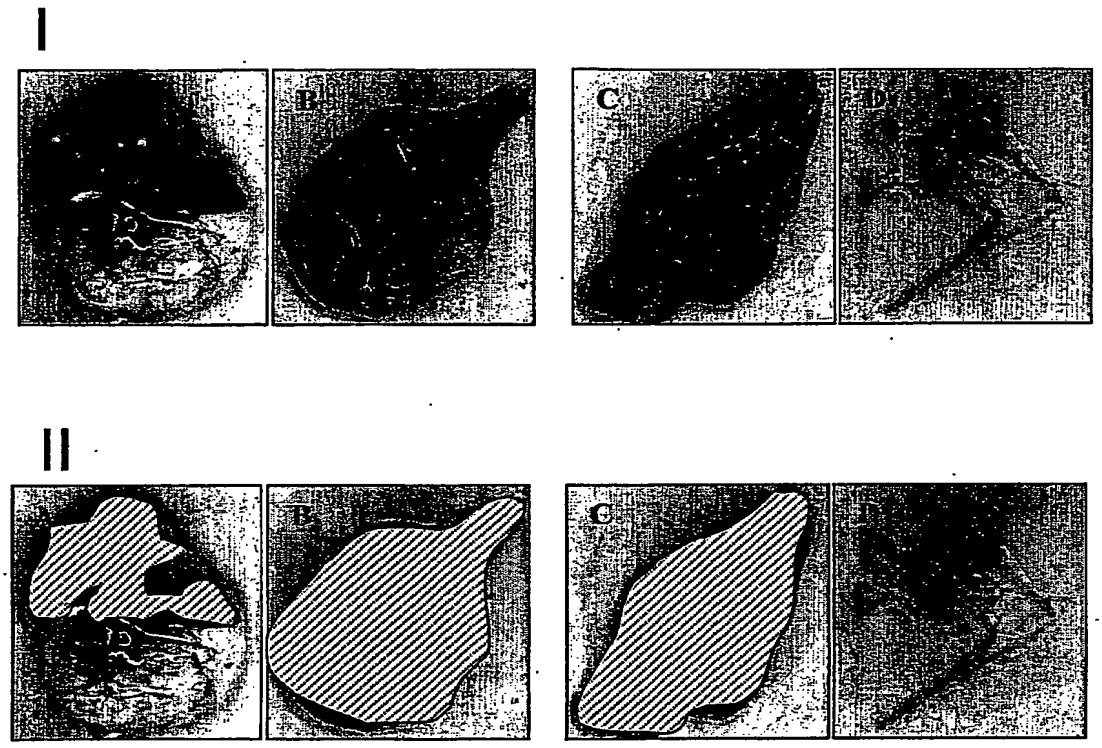

Fig 5

```
                1                                                    50
A           (1) MANFAIANVLILLLNLSTLLNVLACPYCPYPSPKPPTHKPPIVKPPVHK-
B           (1) MANYALANVFILLLNLSTLLIVLACPYCPYPSPKPPTHHPPIVKPPVHKR
C           (1) --------------------------------------------------
D           (1) -PHVKPPSTPKHPKDPPHVKPPSTPKQPPYVKPPTTPKHPPHVKPPS---
E           (1) MGKHGLATWLVILLNFATLLTSLACSYCPSPSPP----------------
F           (1) MGSRVLASFFVFLIFTVITLPPTIQACTPCTRPHPPVPKP----------
Consensus   (1) MA  ALAS   ILLLN STLL  LAC YCPYPSP PP   PP VKPP

               51                                                   100
A          (50) -----------------PPKPQPCPPPSSSPKPPHVPKPPHYPKPPAVHP
B          (51) RKYSPTPKPPVHKPPRYPPKPSPCPPPSSTPKPPHVPKPPHHPKPPVVHP
C           (1) ------------------------------------------RAESART
D          (47) -----------------TPKHPKHPP-----QKPCPPPSHHGPKPPIVKP
E          (35) ----------------------KPP-----KVKHPLPPLPPKHPPHVKP
F          (41) ----------------------PQHGGGGGGGSKPPPHHGGKGGGKPP
Consensus  (51)                     PK    PP     K PH PPP H PKPP VKP

               101                                                  150
A          (83)  PHVPKPP-AVHPPHVPKPPVVHPPIVHPPYVPK-----PPVVKPP-----
B          (101) PHVPKP--PVHPPYVPKPPIVKPPIVHPPYVPK-----PPVVKPPPYVPK
C          (8)   HHMFQP---HPP-YVPKPPIVKPPIVHPPYVPK-----PPVVKPP-----
D          (75)  PHVPRPP-IVHPPPIVSPPSTPKPPKTPPFTPKPPSPIPPIVSPP-----
E          (57)  PHTPMP-------------PNPPAVKPPYVPK-----PPVVEPP-----
F          (67)  PHGGKGGGPPHHGGGGGGGGKSPPVVRPPPVVVRP---PPIIRPP-----
Consensus  (101) PHVPKP    VHPPYVPKPPIV PPIVHPPYVPK    PPVVKPP

               151                                                  200
A          (122) --VVKPPHVPKPPVVPVTPPYIPKPPIVFPPHVPLPP--VVPVTPPYVPK
B          (144) PPVVRPPYVPKPPVVPVTPPYVPKPPVVRPPYVPKPP--VVPVTPPYVPK
C          (44)  --------------------PYVPKPPVVRPPYVPKPP--VVPVTPPYVLS
D          (119) ---------------IVYPPITPTPPIVHPPVTPKPPSPTPPIVSPPIVY
E          (83)  --------------------YVPKPPVVKPPYVPKP-----PVVEPPYMP
F          (109) --------------------PVVYPPPIVRPPPITRPPIIIPPIQPPPVTT
Consensus  (151)                  V PPYVPKPPIVRPPYVPKPP  VVPVTPPYVL

               201                                                  250
A          (168) P-----PIVFPPHVPLPPVVPVTPPYVP-----KPPIVFPPHVPLPPVVP
B          (192) PPIVKPPIVFPPHVPLPPVVPSPPPYVPSPPIVKPPIVFPPHVPLPPVVP
C          (73)  HHCFP-TTVSTSSCTITTTLCTNTPIVN------HQLFFHHMFFYLPVVP
D          (154) PPITPTPPVVSPPIIPTPPIVSPPFVPN------------------PPVV
E          (108) --------------------------------------------------
F          (140) PPGLLPPITTPPG--LLPPVTTPPGLLP---------------PVTTPPG
Consensus  (201) PP    PIV PP V L P V SPPPIVP        I F    PL PVVP

               251                                                  300
A          (208) VTPPYVPLPPVVPVTPPFVPTPPIITPPTPTVPVPSPPSETPCPPPPPTV
B          (242) VTPPYVQPP---PIVTPPTPTPPIVTPPVVSPPTP--PSETPCPPPPLVP
C          (116) VTPPYVQPT--------TYCNSTNTNTSNWTPPTP--PSETLVLPPPLVP
D          (186) IPPPYVPSP------------PVVTPPIVPTPPTPCPP-----PPPPPAI
E          (108) ------------------------------------------------H
F          (173) LLPPIINPP------------PVTVPPPSSGYPPYG---------PPSGG
Consensus  (251) VTPPYVQPP           P IV PP  TPPTP  PSET  PPPP
```

Fig. 6a

```
                  301                                                 350
A           (258) VPYPPPAQPTCSIDALKLGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD
B           (287) YPPTPPAQQTCSIDALKLGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD
C           (156) YP-PPPAQQTCSIDALKLGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD
D           (219) IP-SPPAQPTCPIDALKLGACVDVLGGLIHIGIGGSAKQTCCPLLGGLVD
E           (109) DT----------L---KLGACVDLLGGLVHIGIGSSAKDTCCPVLQGLVD
F           (202) GGGGGGKQPTCPINALKLGACVDVLGGLIHIGLGNPVENVCCPVLQGLLE
Consensus   (301)  P  PPAQPTCSIDALKLGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD

                  351                                           397
A           (308) LDAAVCLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPSS-
B           (337) LDAAICLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPAY-
C           (205) LDAAICLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPAS-
D           (268) LDAAICLCTTIRLKLLNINIILPIALQVLIDDCGKYPPKDFKCPST-
E           (146) LDAAVCLCTAIKVKLLNVNIIIPIALQVLVG-CGKTPPSGFQCPA--
F           (252) LEAAVCLCTTIRLKLLNLNIFIPLALQALIT-CGINPPSGFVCPPLT
Consensus   (351) LDAAICLCTTIRLKLLNINIVIPLALQVLID CGKTPPEGFKCPAS
```

Fig. 6b

```
                 551                                                 600
B           (551) AAAAACTAAAAAATAATTTCTCTCCTGATTTATATGAAATGACATTTTTT
A           (1)   ----------------------------------------CGCAATTTTTT
Consensus   (551)                                          G  ATTTTTT
                 601                                                 650
B           (601) TGGAACATGAAGG-GTATTGATTTTTACCACCTTTTACACCT--TTCAAA
A           (12)  GTGAAGCTGAGGGAGGATTGGATTTTACACCTATTCAAAAGTCATTCAAA
Consensus   (601)   GAA  TGA GG G ATTG  TTTTAC  C  TT A A  T  TTCAAA
                 651                                                 700
B           (648) G----------CCATTCAAGGATGAATATAGATTTTTGGGCGATCAAACAC
A           (62)  GTTTGTCCCTCCATTCAAGGATGAATGTAGATTTTTCAAGCATCAAACAC
Consensus   (651) G          CCATTCAAGGATGAAT TAGATTTTT     ATCAAACAC
                 701                                                 750
B           (689) AAGAATCATTACGATAACATGCTTTGGAACACACACATGCTTAAATTAAT
A           (112) AAGAATCACTAGCATAACATGCTTTGAAACCCACACA--CTTAAATTAAT
Consensus   (701) AAGAATCA TA  ATAACATGCTTTG AAC CACACA  CTTAAATTAAT
                 751                                                 800
B           (739) GGTTGGAGTATCAAAT----TTTAAAAT-ATTGTTGTCAAT-ACATACCC
A           (160) GTTAGGAATATCAAATCCAATATAAAATCATAGTTGTCAATTACATACTC
Consensus   (751) G T GGA TATCAAAT    T TAAAAT AT GTTGTCAAT ACATAC C
                 801                                                 850
B           (783) CGTCAATCTTCTTTTTTTTACCCAATAAACATTGAAATGTTGCTTCTTTC
A           (210) AATCAAGTCCCTTTCTTTTACCCAATAAACATCAACATATTGCTTCTTCC
Consensus   (801)   TCAA     CTTT TTTTACCCAATAAACAT  A AT TTGCTTCTT C
                 851                                                 900
B           (833) GTTAAGCATAAAAACATCAAAGTCTA------GCAAAATGTTGTTTTTGC
A           (260) ATTAAGCATATAAACATCAAAGTCTAAAACTAGCAAAATGTTGTTTTTAG
Consensus   (851)  TTAAGCATA AAACATCAAAGTCTA      GCAAAATGTTGTTTTT
                 901                                                 950
B           (877) GATGACACATTTCATA--TAGTTTAAAGGATGCATGATTCGATTACAAAA
A           (310) GATGACACATTTCATACATAGTTTAAAAGATACTTGATTCGATTACAAAA
Consensus   (901) GATGACACATTTCATA  TAGTTTAAA GAT C TGATTCGATTACAAAA
                 951                                                1000
B           (925) ACAAAATACTAATAATTCTAGCACAAAGTTTAAAGCAAGATTATAAAGCT
A           (360) AGAAATTACCAATAGTT-TAGCACAAAGTCTAAAGCATAATTA--AAGCA
Consensus   (951) A AAA TAC AATA TT TAGCACAAAGT TAAAGCA  ATTA  AAGC
                1001                                                1050
B           (975)  TCATAGCATGTGGATATTCATTTAGAAATATAGATTA-GATTGCCCCTTT
A           (407)  TCA---CATGTGCAGATTTAT---GAAAAAAAGATTAAGATTGCCCCTTT
Consensus   (1001) TCA   CATGTG A ATT AT   GAAA A AGATTA GATTGCCCCTTT
                1051                                                1100
B           (1024) CATCACGGGTC---TAACAGCACCACTTGTCACTACATGTCAAAAA--TG
A           (451)  CATCACGGGTCGAATAATAGCACTACTTGTCACTACATGTTAAAAAAATG
Consensus   (1051) CATCACGGGTC   TAA AGCAC ACTTGTCACTACATGT AAAAA  TG
                1101                                                1150
B           (1069) TCCTCTAGTACAGCACCGCTTTTTACTTGATTCCCCTTGTCCATGCATGA
A           (501)  TCCTCTAGTACATCAAACTTTTTCCATTGATTCCCCTTATCC----ATGA
Consensus   (1101) TCCTCTAGTACA CA    TTTT   TTGATTCCCCTT TCC    ATGA
                1151                                                1200
B           (1119) AAAAAATCAAAACAATATTTGGACACACAAACTTGCCCCCACTTTCCTTT
A           (547)  AAAAAATAAACAAATTCTTAAGACACAAAAAAATGGCCCCACAT-CCTTT
Consensus   (1151) AAAAAAT AA A A T TT  GACACA AAA  TG CCCCAC T CCTTT
```

Fig. 7a

```
                    1201                                                1250
B           (1169) TTCTTTCTGCCCTAGTTTGTTTGAGACTCATATTGATCAAATTTGGCTAT
A           (596)  ---TTTCTGGCCTAGTTTGTTTGA-------------------------
Consensus   (1201)    TTTCTG CCTAGTTTGTTTGA
                    1251                                                1300
B           (1219) GAATTCAAACAAAAAATTCACTCTACCCATTGCATGTGT---GGGGCCCA
A           (617)  -----------A----TTCATTCTAACTCTTGAATATGTAACGAGGCCCA
Consensus   (1251)           A    TTCA TCTA C  TTG AT TGT   G GGCCCA
                    1301                                                1350
B           (1266) CATATAAATCCATGAAGGATTTCAATGTCCATCCAAGTCAATGATTCAAC
A           (652)  C-TAAAAATCAAT------------------------CAATGATTTAAC
Consensus   (1301) C TA AAATC AT                        CAATGATT AAC
                    1351                                                1400
B           (1316) ATATATAACATTGAATAATTTAATTCCAATTTGCAGTATTATGATTTAGA
A           (676)  ATAAAAAA---TGAATAGTTTAATTCCAATTTGC----------------
Consensus   (1351) ATA A AA   TGAATA TTTAATTCCAATTTGC
                    1401                                                1450
B           (1366) TTGATTGCTGCAATACGGTCCGTGAATGTGATCACTCACGAGAAAGAGGT
A           (707)  --------TGCAACATGGTCCGTGAATATGA---CTCACGAGAAAGATAT
Consensus   (1401)         TGCAA A GGTCCGTGAAT TGA   CTCACGAGAAAGA T
                    1451                                                1500
B           (1416) ATCAAAATTTCAAGGTATTTTATTTATTTTTAACAAATAAAATTTCAAGG
A           (746)  ATCAAAATATCAA-------------------------AATTTCATAG
Consensus   (1451) ATCAAAAT TCAA                          AATTTCA  G
                    1501                                                1550
B           (1466) TCTTGTTCACCATATAAACCTCCTCACTCACACCCAATTCTCTTAAGTGT
A           (769)  TTTTTTTCACCATATAAACCTCATCACTCATTC--TATTTTTTTAAGTGC
Consensus   (1501) T TT TTCACCATATAAACCTC TCACTCA  C   ATT T TTAAGTG
                    1551                                                1600
B           (1516) ATGACTTCATAGTAC--ACTACACTACTTTCTTTGAAACATGGCTAACTA
A           (817)  AAAGCTTCATAGTAGTGAGCACACACATTACACTAAAATCTTCGAAACTT
Consensus   (1551) A   CTTCATAGTA   A  ACAC   TT C  T AAA  T    AACT
                    1601                                                1650
B           (1564) TGCTCTAGCCAATGTTTTCATCCTTCTCTTGAACTTGAGTACCTTACTCA
A           (867)  A-----------------------------------------------
Consensus   (1601)
```

Fig. 7b

```
                          1                                                  50
SEQ ID NO: 9   (1)  ---CTTTTCAACAATCATGCCCATGTCAAGTGTAAAACAGGTTTACCTCT
SEQ ID NO: 8   (1)  AAGCTTTTCAACAATCATGCCCATGTCAAGTGTAAAACAGGTTTACCTCT
SEQ ID NO: 7   (1)  AAGCTTTTCAACAATCATGCCCATGTCAAGTGTAAAACAGGTTTACCTCT
Consensus      (1)  AAGCTTTTCAACAATCATGCCCATGTCAAGTGTAAAACAGGTTTACCTCT
                         51                                                 100
SEQ ID NO: 9  (48)  CTTAAATAACCGTATTAAAATGCTGAATGATGTATATATGTGGGTTCAAA
SEQ ID NO: 8  (51)  CTTAAATAACCGTATTAAAATGCTGAATGATGTATATATGTGGGTTCAAA
SEQ ID NO: 7  (51)  CTTAAATAACCGTATTAAAATGCTGAATGATGTATATATGTGGGTTCAAA
Consensus     (51)  CTTAAATAACCGTATTAAAATGCTGAATGATGTATATATGTGGGTTCAAA
                        101                                                 150
SEQ ID NO: 9  (98)  TTACATAATTTGTAAGTATGTTACACATTGTATAAATATGTTTTAGAGAA
SEQ ID NO: 8(101)  TTACATAATTTGTAAGTATGTTACACATTGTATAAATATGTTTTAGAGAA
SEQ ID NO: 7(101)  TTACATAATTTGTAAGTATGTTACACATTGTATAAATATGTTTTAGAGAA
Consensus    (101)  TTACATAATTTGTAAGTATGTTACACATTGTATAAATATGTTTTAGAGAA
                        151                                                 200
SEQ ID NO: 9(148)  AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT
SEQ ID NO: 8(151)  AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT
SEQ ID NO: 7(151)  AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT
Consensus    (151)  AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT
                        201                                                 250
SEQ ID NO: 9(198)  TTCAGTTAAGATTTAAATAGTATAAATTAAAAATTATCGATGATGACAAA
SEQ ID NO: 8(201)  TTCAGTTAAGATTTAAATAGTATAAATTAAAAATTATCGATGATGACAAA
SEQ ID NO: 7(201)  TTCAGTTAAGATTTAAATAGTATAA-TTAAAAATTATCGATGATGACAAA
Consensus    (201)  TTCAGTTAAGATTTAAATAGTATAAATTAAAAATTATCGATGATGACAAA
                        251                                                 300
SEQ ID NO: 9(248)  AAATTGTAAATATAATTCATTTTAAAAAAAGTTAAGAAATTGAAAAAGGA
SEQ ID NO: 8(251)  AAATTGTAAATATAATTCATTTTAAAAAAAGTTAAGAAATTGAAAAAGGA
SEQ ID NO: 7(250)  AAATTGTAAATATAATTCATTTTAAAAAAAGTTAAGAAATTGAAAAAGGA
Consensus    (251)  AAATTGTAAATATAATTCATTTTAAAAAAAGTTAAGAAATTGAAAAAGGA
                        301                                                 350
SEQ ID NO: 9(298)  AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA
SEQ ID NO: 8(301)  AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA
SEQ ID NO: 7(300)  AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA
Consensus    (301)  AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA
                        351                                                 400
SEQ ID NO: 9(348)  TATATATGTATATTTTATTTTTGACTGAATATATGTGTGTATAGACAATA
SEQ ID NO: 8(351)  TATATATGTATATTTTATTTTTGACTGAATATATGTGTGTATAGACAATA
SEQ ID NO: 7(350)  TATATATGTATATTTTATTTTTGACTGAATATATGTGTGTATAGACAATA
Consensus    (351)  TATATATGTATATTTTATTTTTGACTGAATATATGTGTGTATAGACAATA
                        401                                                 450
SEQ ID NO: 9(398)  ATGCGCAGAATGCCGATCGATGAATTGTTTACTGCATTTCCAAATATGTG
SEQ ID NO: 8(401)  ATGCGCAGAATGCCGATCGATGAATTGTTTACTGCATTTCCAAATATGTG
SEQ ID NO: 7(400)  ATGCGCAGAATGCCGATCGATGAATTGTTTACTGCATTTCCAAATATGTG
Consensus    (401)  ATGCGCAGAATGCCGATCGATGAATTGTTTACTGCATTTCCAAATATGTG
                        451                                                 500
SEQ ID NO: 9(448)  TGCATAAGCGTTCCACATGTCACCCATGTTGTAATTAGTTTCTTCCCTGG
SEQ ID NO: 8(451)  TGCATAAGCGTTCCACATGTCACCCATGTTGTAATTAGTTTCTTCCCTGG
SEQ ID NO: 7(450)  TGCATAAGCGTTCCACATGTCACCCATGTTGTAATTAGTTTCTTCCCTGG
Consensus    (451)  TGCATAAGCGTTCCACATGTCACCCATGTTGTAATTAGTTTCTTCCCTGG
                        501                                                 550
```

Fig. 8a

```
SEQ ID NO: 9(498) ATGAATTACTAAGAAACAGATTGATTGATAGTACTATATTAAATTATGTA
SEQ ID NO: 8(501) ATGAATTACTAAGAAACAGATTGATTGATAGTACTATATTAAATTATGTA
SEQ ID NO: 7(500) ATGAATTACTAAGAAACAGATTGATTGATAGTACTATATTAAATTATGTA
Consensus   (501) ATGAATTACTAAGAAACAGATTGATTGATAGTACTATATTAAATTATGTA
                  551                                             600
SEQ ID NO: 9(548) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT
SEQ ID NO: 8(551) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT
SEQ ID NO: 7(550) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT
Consensus   (551) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT
                  601                                             650
SEQ ID NO: 9(598) AGGAAGTCACAGACAATTTGAAGACAATTTCTTTAGCTTACCTATCTCAT
SEQ ID NO: 8(601) AGGAAGTCACAGACAATTTGAAGACAATTTCTTTAGCTTACCTATCTCAT
SEQ ID NO: 7(600) AGGAAGTCACAGACAATTTGAAGACAATTTCTTTAGCTTACCTATCTCAT
Consensus   (601) AGGAAGTCACAGACAATTTGAAGACAATTTCTTTAGCTTACCTATCTCAT
                  651                                             700
SEQ ID NO: 9(648) GCCACAATTATGTACTTACGACAGTAAAATGTTTAAAAGCAAAA------
SEQ ID NO: 8(651) GCCACAATTATGTACTTACGACAGTAAAATGTTTAAAAGCAAAA------
SEQ ID NO: 7(650) GCCACAATTATGTACTTACGACAGTAAAATGTTTAAAAGCAAAAGCAAAA
Consensus   (651) GCCACAATTATGTACTTACGACAGTAAAATGTTTAAAAGCAAAA
                  701                                             750
SEQ ID NO: 9(692) AAAAGAAAGAAGAAGAAGAAGTAATAAATGGAATTATATAGAATGTACTC
SEQ ID NO: 8(695) AAAAGAAAGAAGAAGAAGAAGTAATAAATGGAATTATATAGAATGTACTC
SEQ ID NO: 7(700) AAAAGAAAGAAGAAGAAGAAGTAATAAATGGAATTATATAGAATGTACTC
Consensus   (701) AAAAGAAAGAAGAAGAAGAAGTAATAAATGGAATTATATAGAATGTACTC
                  751                                             800
SEQ ID NO: 9(742) TTTGTCTTCATCTGCCCTATAATTCCTGCAGCAGCCAAAGCATAATAGCA
SEQ ID NO: 8(745) TTTGTCTTCATCTGCCCTATAATTCCTGCAGCAGCCAAAGCATAATAGCA
SEQ ID NO: 7(750) TTTGTCTTCATCTGCCCTATAATTCCTGCAGCAGCCAAAGCATAATAGCA
Consensus   (751) TTTGTCTTCATCTGCCCTATAATTCCTGCAGCAGCCAAAGCATAATAGCA
                  801                                             850
SEQ ID NO: 9(792) TGCAATATGCACATATTCGTTTTAGGCTTTTAGCCTCCACGATCTGTTAA
SEQ ID NO: 8(795) TGCAATATGCACATATTCGTTTTAGGCTTTTAGCCTCCACGATCTGTTAA
SEQ ID NO: 7(800) TGCAATATGCACATATTCGTTTTAGGCTTTTAGC-TCCACGATCTGTTAA
Consensus   (801) TGCAATATGCACATATTCGTTTTAGGCTTTTAGCCTCCACGATCTGTTAA
                  851                                             900
SEQ ID NO: 9(842) TGGAAAGTGAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC
SEQ ID NO: 8(845) TGGAAAGTGAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC
SEQ ID NO: 7(849) TGGAAAGTGAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC
Consensus   (851) TGGAAAGTGAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC
                  901                                             950
SEQ ID NO: 9(892) CAGGGAAGCACTAGAAGATATGAAATGACATAAAAGGTCACCATGCATAA
SEQ ID NO: 8(895) CAGGGAAGCACTAGAAGATATGAAATGACATAAAAGGTCACCATGCATAA
SEQ ID NO: 7(899) CAGGGAAGCACTAGAAGATATGAAATGAC-TAAAAGGTCACCATGCATAA
Consensus   (901) CAGGGAAGCACTAGAAGATATGAAATGACATAAAAGGTCACCATGCATAA
                  951                                            1000
SEQ ID NO: 9(942) TGCTTTAAATGCTTGCTATAGAATCAAAAAATGAAGAGATGTGACAAATT
SEQ ID NO: 8(945) TGCTTTAAATGCTTGCTATAGAATCAAAAAATGAAGAGATGTGACAAATT
SEQ ID NO: 7(948) TGCTTTAAATGCTTGCTATAGAATCAAAAAATGAAGAGATGTGACAAATT
Consensus   (951) TGCTTTAAATGCTTGCTATAGAATCAAAAAATGAAGAGATGTGACAAATT
```

Fig. 8b

```
                    1001                                                1050
SEQ ID NO: 9(992)  GTTACATCTAATACGCAATAATTTGACAAAGACGACTATGCGTTTATATA
SEQ ID NO: 8(995)  GTTACATCTAATACGCAATAATTTGACAAAGACGACTATGCGTTTATATA
SEQ ID NO: 7(998)  GTTACATCTAATACGCAATAATTTGACAAAGACGACTATGCGTTTATATA
Consensus  (1001)  GTTACATCTAATACGCAATAATTTGACAAAGACGACTATGCGTTTATATA
                    1051                                                1100
SEQ ID NO: 9(1042)  TTTATTTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG
SEQ ID NO: 8(1045)  TTTATTTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG
SEQ ID NO: 7(1048)  TTTATTTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG
Consensus   (1051)  TTTATTTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG
                    1101                                                1150
SEQ ID NO: 9(1092)  TCAACATTTCCAGGCAACTAGTTAGTTATTTTATTTTCTTGTTTATAATT
SEQ ID NO: 8(1095)  TCAACATTTCCAGGCAACTAGTTAGTTATTTTATTTTCTTGTTTATAATT
SEQ ID NO: 7(1098)  TCAACATTTCCAGGCAACTAGTTAGTTATTTTATTTTCTTGTTTATAATT
Consensus   (1101)  TCAACATTTCCAGGCAACTAGTTAGTTATTTTATTTTCTTGTTTATAATT
                    1151                                                1200
SEQ ID NO: 9(1142)  ATTTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTTCCACAA
SEQ ID NO: 8(1145)  ATTTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTTCCACAA
SEQ ID NO: 7(1148)  ATTTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCGTTCCACAA
Consensus   (1151)  ATTTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTTCCACAA
                    1201                                                1250
SEQ ID NO: 9(1192)  CCAACTTGGTCGCATTGGTCCAAAAAACTCAATATCAATATTTTCGAAAT
SEQ ID NO: 8(1195)  CCAACTTGGTCGCATTGGTCCAAAAAACTCAATATCAATATTTTCGAAAT
SEQ ID NO: 7(1198)  CCAACTTGGT---------CCAAAAAACTCAATATCAATATTTTCAAAAT
Consensus   (1201)  CCAACTTGGTCGCATTGGTCCAAAAAACTCAATATCAATATTTTCGAAAT
                    1251                                                1300
SEQ ID NO: 9(1242)  AGTTTTAGCATTGTTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC
SEQ ID NO: 8(1245)  AGTTTTAGCATTGTTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC
SEQ ID NO: 7(1239)  AGTTTTAGCATTGTTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC
Consensus   (1251)  AGTTTTAGCATTGTTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC
                    1301                                                1350
SEQ ID NO: 9(1292)  TCCACCTACCAAGATAAAATAGTTGGATAAATGGGTAAAAAAAGTTGTAT
SEQ ID NO: 8(1295)  TCCACCTACCAAGATAAAATAGTTGGATAAATGGGTAAAAAAAGTTGTAT
SEQ ID NO: 7(1289)  TCCACCTACCAAGATAAAATAGTTGGATAAATGGGTAAAAAA-GTTGTAT
Consensus   (1301)  TCCACCTACCAAGATAAAATAGTTGGATAAATGGGTAAAAAAAGTTGTAT
                    1351                                          1393
SEQ ID NO: 9(1342)  AAAGGGCAACACTACCTCTCCTAATGGCAGTA-----------
SEQ ID NO: 8(1345)  AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAAACCCAAG
SEQ ID NO: 7(1338)  AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAAACCCAAG
Consensus   (1351)  AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAAACCCAAG
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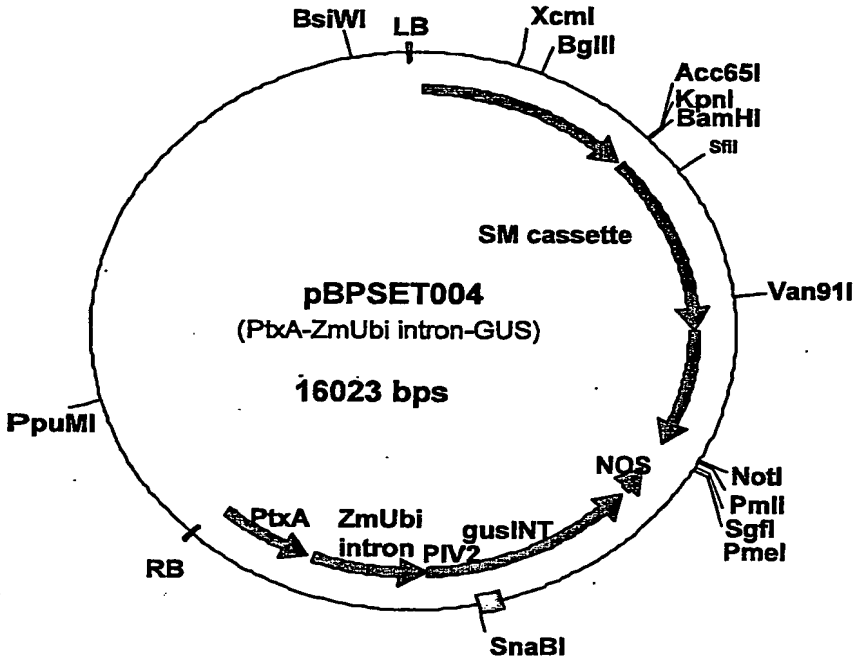
Fig. 8c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PmlI
SgfI
PmeI
PtxA
ZmUbi
intron
gusINT
PIV2
RB
SnaBI

Fig. 9